

SEQ ID No 1. - HCV Core Protein

GTGCCCCTTCAGCCTACCAAGTGCGCAAC 930
CACGGGCGAAGTCGGATGGTTCACGCGTTG
V P A S A Y Q V R N 196

[illegible]

ACCCTTACGTGCGGCTTCGTCGATCTCATGGGGTACATAACCGCTCGTCGGCGCCCCTCTT 777
TGGGAATGCACGCCGAAGCAGCTAGAGTACCCCATGTATGGCGAGCAGCCGCGGGGAGAA
T L T C G F V D L M G Y I P L V G A P L 144

GGTGTGA ACTATGCAACA 840
CCACACTTGATACGTTGT
G V N Y A T 166

CGTCTTCGGGACGCGCCCGCTCTTCGCCTTTCGCTGCAGTCCGTCGATTTCTTTCTCCAG	60
GAAGAAAAATGGCATCCGTTGCAGTTGATCCACAACCGAGTGTGGTGACTCGGGTGGTCA	120
ACCTGCCCTTGGTGAGCTCCACGTATGACCTCATGTCCTCAGCCTATCTCAGTACAAAGG	180
ACCAGTATCCCTACCTGAAGTCTGTGTGTGAGATGSCAGAGAACGGTGTGAAGACCATCA	240
CCTCCGTGGCCATGACCAGTGCTCTGCCCATCATCCAGAAGCTAGAGCCGCAAATTGCAG	300
TTGCCGATACCTATGCCTGTAAGGGGCTAGACAGGATTGAGGAGAGACTGCCTATTCTGA	360
ATCAGCCATCAACTCAGATTGTTGCCAATGCCAAAGGCGCTGTGACTGGGGCAAAGATG	420
CTGTGACGACTACTGTGACTGGGGCCAAGGATTCTGTNGCCAGCACGATCACAGGGGTGA	480
TGGACAAGACCAAAGGGGCAGTGACTGGCAGTGTGGAGAAGACCAAGTCTGTGGTCAGTG	540
GCAGCATTAACACAGTCTTGGGGAGTCGGATGATGCAGCTCGTGAGCAGTGGCGTAGAAA	600
ATGCACTCACCAAATCAGAGCTGTTGGTAGAACAGTACCTCCCTCTCACTGAGGAAGAAC	660
TAGAAAAAGAAGCAAAAAAAGTTGAAGGATTTGATCTGGTTTCAGAAAGCCAAGTTATTATG	720
TTAGACTGGGATCCCTGTCTACCAAGCTTCACTCCCGTGCCTACCAGCAGGCTCTCAGCA	780
GGGTAAAGAAGCTAAGCAAAAAAGCCAACAGACCATTTCTCAGCTCCATTCTACTGTTC	840
ACCTGATTGAATTTGCCAGGAAGAATGTGTATAGTGCCAATCAGAAAATTGAGGATGCTC	900
AGGATAAGCTCTACCTCTCATGGGTAGAGTGGAAGGAGCATTGGATATGATGATACTG	960
ATGAGTCCCAGTGTGCTGAGCACATTGAGTCACGTACTCTTGCAATTGCCCCGAACCTGA	1020
CTCAGCAGCTCCAGACCACGTGCCACACCCTCCTGTCCAACATCCAAGGTGTACCACAGA	1080
ACATCCAAGATCAAGCCAAGCACATGGGGGTGATGGCAGGCGACATCTACTCAGTGTTCC	1140
GCAATGCTGCCTCCTTTAAAGAAGTGTCTGACAGCCTCCTCACTTCTAGCAAGGGGCAGC	1200
TGCAGAAAATGAAGGAATCTTTAGATGACGTGATGGATTATCTTGTTAACAACACGCCCC	1260
TCAACTGGCTGGTAGGTCCCTTTTATCCTCAGCTGACTGAGTCTCAGAATGCTCAGGACC	1320

[illegible]

[illegible]

MetAlaSerValAlaValAspProGlnProSerValValThrArgVal	16
ValAsnLeuProLeuValSerSerThrTyrAspLeuMetSerSerAla	32
TyrLeuSerThrLysAspGlnTyrProTyrLeuLysSerValCysGlu	48
MetXaaGluAsnGlyValLysThrIleThrSerValAlaMetThrSer	64
AlaLeuProIleIleGlnLysLeuGluProGlnIleAlaValAlaAsp	80
ThrTyrAlaCysLysGlyLeuAspArgIleGluGluArgLeuProIle	96
LeuAsnGlnProSerThrGlnIleValAlaAsnAlaLysGlyAlaVal	112
ThrGlyAlaLysAspAlaValThrThrThrValThrGlyAlaLysAsp	128
SerValAlaSerThrIleThrGlyValMetAspLysThrLysGlyAla	144
ValThrGlySerValGluLysThrLysSerValValSerGlySerIle	160
AsnThrValLeuGlySerArgMetMetGlnLeuValSerSerGlyVal	176
GluAsnAlaLeuThrLysSerGluLeuLeuValGluGlnTyrLeuPro	192
LeuThrGluGluGluLeuGluLysGluAlaLysLysValGluGlyPhe	208
AspLeuValGlnLysProSerTyrTyrValArgLeuGlySerLeuSer	224
ThrLysLeuHisSerArgAlaTyrGlnGlnAlaLeuSerArgValLys	240
GluAlaLysGlnLysSerGlnGlnThrIleSerGlnLeuHisSerThr	256
ValHisLeuIleGluPheAlaArgLysAsnValTyrSerAlaAsnGln	272
LysIleGlnAspAlaGlnAspLysLeuTyrLeuSerTrpValGluTrp	288
LysArgSerIleGlyTyrAspAspThrAspGluSerHisCysAlaGlu	304
HisIleGluSerArgThrLeuAlaIleAlaArgAsnLeuThrGlnGln	320

LeuGlnThrThrCysHisThrLeuLeuSerAsnIleGlnGlyValPro	336
GlnAsnIleGlnAspGlnAlaLysHisMetGlyValMetAlaGlyAsp	352
IleTyrSerValPheArgAsnAlaAlaSerPheLysGluValSerAsp	368
SerLeuLeuThrSerSerLysGlyGlnLeuGlnLysMetLysGluSer	384
LeuAspAspValMetAspTyrLeuValAsnAsnThrProLeuAsnTrp	400
LeuValGlyProPheTyrProGlnLeuThrGluSerGlnAsnAlaGln	416
AspGlnGlyAlaGluMetAspLysSerSerGlnGluThrGlnArgSer	432
GluHisLysThrHis	437